Amendments to the Specification

1. Please replace the existing Sequence Listing with the enclosed Replacement Sequence Listing (9 pages).

2. Please amend the paragraph at page 4, line 14, as follows:

Figure 1: Similarity of PAGE-4, GAGE and MAGE: (A) The predicted PAGE-4 reading frame (SEQ ID NO: 1) is derived from the full length PAGE-4 EST clone nh32c06. The GAGE and MAGE sequences are from SW: GGE1 (SEQ ID NO: 2), GGE2 (SEQ ID NO: 3), GGE3 (SEQ ID NO: 4), GGE4 (SEQ ID NO: 5), GGE5 (SEQ ID NO: 6), GGE6 (SEQ ID NO: 7), MAG5 (SEQ ID NO: 8) and MAG8_HUMAN (SEQ ID NO: 9). Note that the "MAGE-alignment" matches amino acids that occur in MAGE5 and/or MAGE8, which are similar to PAGE-4 and/or GAGE1-6; the homologies between single members of the MAGE and PAGE and GAGE protein families are weaker. (B) Alignment of [[PAGE-4]] PAGE-1 (SEQ ID NO: 10) with other PAGEs. PAGE-2 (SEQ ID NO: 11) was translated from the EST ai61a04 EST-cluster and PAGE-3 from om29f08. PAGE-3 (SEQ ID NO: 12) was translated from one single EST and it is possible that the truncated amino terminus results from a sequence artifact (the homology extends further to the N-terminus in another reading frame). Several other so far undefined EST clusters were found that have homology to PAGE as well as to GAGE. These clusters do not have the striking similarities that the other GAGE family members have to each other, but they are also not significantly more similar to PAGE than to GAGE. Representatives of some of these cDNA clusters are the ESTS yd88e11 (fetal liver/spleen), yw86a06 (placenta) and yi21h01 (placenta).

3. Please amend the paragraph at page 5, line 21, as follows:

Figure 5: Nucleotide sequence encoding PAGE-4 (SEQ ID NO: 13): The open reading frame is in bold type and underlined.

4. Please amend the paragraph at page 30, line 22, as follows:

In preferred embodiments of the present invention, the toxin is *Pseudomonas* exotoxin (PE). The term "*Pseudomonas* exotoxin" as used herein refers to a full-length native (naturally occurring) PE or a PE that has been modified. Such modifications may include, but are not limited to, elimination of domain Ia, various amino acid deletions in domains Ib, II and III, single amino acid substitutions and the addition of one or more sequences at the carboxyl terminus such as KDEL (SEQ ID NO: 14) and REDL (SEQ ID NO: 15). *See* Siegall, *et al., J. Biol. Chem.* **264**:14256 (1989). In a preferred embodiment, the cytotoxic fragment of PE retains at least 50%, preferably 75%, more preferably at least 90%, and most preferably 95% of the cytotoxicity of native PE. In a most preferred embodiment, the cytotoxic fragment is more toxic than native PE.

5. Please amend the paragraph at page 41, line 12, as follows:

An exemplary PAGE-4 peptide was selected to demonstrate that the PAGE-4 protein could be used to generate antibodies. The sequence used was, in single letter code, EGTPPIEERKVEGDC (SEQ ID NO: 16).